6. (Amended) The phosphoprotein (P) protein of Newcastle disease virus (NDV) encoded by the nucleic acid molecule of claim 3 or claim 4, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 4.

15. (Amended) A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 3.

16. (Amended) A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14, wherein the protein comprises the amino acid set forth as SEQ ID NO: 4.

## Remarks

Applicants have amended the claims and specification to include the sequence identification numbers for the sequences in the claims and have amended the claims for clarification. No new matter has been added by this amendment. Applicants also hereby request the entry of the sequence listing into the application.

If the amendment is defective or unclear, the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

John R. Van Amsterdam

Reg. No. 40,212

Wolf, Greenfield & Sacks, P.C.

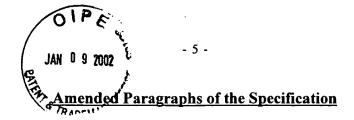
600 Atlantic Avenue

Boston, MA 02210-2211

(617) 720-3500

Docket No. S1436/7007 Date: January 9, 2002

X1/09/02



Page 3, line 5.

NP coding region <(SEQ ID NO: 1)>

Page 5, line 3.

P gene coding region <(SEQ ID NO: 2)>

Page 6, line 19.

NP gene <(SEQ ID NO: 1)>: amino acid sequence <(SEQ ID NO: 3)>

Page 9, line 23.

P gene <(SEQ ID NO: 2)>: amino acid sequence <(SEQ ID NO: 4)>

Page 13, lines 11 through 18.

For the amplification of the NP gene

NPf1 (20 mer): 5'- cct tct gcc aac atg tct tc -3' (Forward primer<; SEQ ID NO: 5>)

NPr1 (20 mer): 5'- tca ata ccc cca gtc ggt gt -3' (Reverse primer<; SEQ ID NO: 6>)

NPr2 (18 mer): 5'- ata ccc cca gtc ggt gtc -3' (Reverse primer<; SEQ ID NO: 7>)

For the amplification of the P gene

Pf1 (20 mer): 5'- atg gcc acc ttt aca gat gc -3' (Forward primer<; SEQ ID NO: 8>)

Pr1 (23 mer): 5'- taa tta gcc att tag tgc aag gc -3' (Reverse primer<; SEQ ID NO: 9>)

Pr2 (21 mer): 5'- gcc att tag tgc aag gcg ctt -3' (Reverse primer<; SEQ ID NO: 10>)

Page 14, lines 13 through 27.

For the sequencing of the NP gene coding region

PTrcHis2F (21 mer): 5'- gag gta tat att aat gta tcg -3' <(SEQ ID NO: 11)>

SNPf1 (21 mer): 5'- gac tca tac atc agg aac acc -3' <(SEQ ID NO: 12)>

SNPf2 (21 mer): 5'- gat gag agc agt ggc gaa cag -3' <(SEQ ID NO: 13)>

PTrcHis2R (18 mer): 5'- gat tta atc tgt atc agg -3' <(SEQ ID NO: 14)>

SNPr1 (20 mer): 5'- tca ata ccc cca gtc ggt gt -3' <(SEQ ID NO: 15)> sNPr2 (21 mer): 5'- cta agt tgt aat acg tgg agc -3' <(SEQ ID NO: 16)> sNPr3 (21 mer): 5'- cca tcg atc tca aga aca tgc -3' <(SEQ ID NO: 17)>

For the sequencing of the P gene coding region

pTrcHis2F (21 mer): 5'- gag gta tat att aat gta tcg -3' <(SEQ ID NO: 18)>
sPf1 (21 mer): 5'- gtc gac ttt gtg cag gcg atg -3' <(SEQ ID NO: 19)>
sPf2 (21 mer): 5'- gga cac tgt ccg tgc att gat -3' <(SEQ ID NO: 20)>
pTrcHis2.R (18 mer): 5'- gat tta atc tgt atc agg -3' <(SEQ ID NO: 21)>
sPr1 (21 mer): 5'- cca ggg tcc aga att ttc atc -3' <(SEQ ID NO: 22)>
sPr2 (22 mer): 5'- ggt gtg gat agc tgt ttg tct g -3' <(SEQ ID NO: 23)>

## **Amended Claims**

- 1. (Amended) <A nucleic acid molecule>[Nucleotides] encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).
- 2. (Amended) The [nucleotides as claimed in] <nucleic acid molecule of> claim 1<, wherein the nucleic acid molecule comprises the nucleotide sequence set forth as SEQ ID NO: 1.> [characterised in that it has the following nucleotide sequence:

ATGTCTTCCG TATTCGATGA ATACGAGCAG CTCCTCGCTG CTCAGACTCG CCCCAATGGA GCTCACGGAG GGGGAGAGA AGGGAGCACT TTAAGAGTTG AGGTCCCAGT ATTCACTCTT AACAGTGACG ATCCAGAAGA TAGATGGAAT TTTGCGGTAT TCTGTCTTCG GATTGCTGTT AGCGAGGACG CCAACAACC GCTCAGGCAA GGTGCTCTCA TATCCCTCCT GTGCTCCCAT TCTCAAGTGA TGAGGAACCA TGTTGCCCTT GCAGGAAAAC AGAATGAGGC TACACTGACT GTTCTTGAGA TCGATGGTTT TACCAGCAGC GTGCCTCAGT TCAACAACAG GAGTGGGGTG 

TCTGAGGAGA	GAGCACAGAG	ATTCATGGTG	ATAGCAGGGT	CTCTCCCTCG	GGCGTGCAGT
430	440	450	460	470	480
AACGGTACTC	CGTTCGTCAC	GGCTGGGGTT	GAAGATGATG	CACCAGAAGA	TATCACTGAT
490	500	510		530	540
ACTCTGGAAA	GAATCCTGTC	TATCCAGGCT		TCACAGTAGC	GAAGGCCATG
550	560	570		590	600
ACTGCATATG	AGACAGCAGA	TGAGTCGGAA		TCAATAAGTA	CATGCAGCAA
610	620	630	640	650	660
GGCAGAGTCC	AGAAGAAGTA	CATCCTCCAC	CCTGTATGCA	GGAGTGCAAT	TCAACTCACA
670 ATCAGACATT	680 CTCTGGCAGT			710 AGCTTAAGAG	720 AGGCCGCAAT
730	740	750	760	770	780
ACGGCAGGTG	GGAGCTCCAC	GTATTACAAC	TTAGTAGGGG	ATGTAGACTC	ATACATCAGG
790	800	810	820	830	840
AACACCGGAC	TTACTGCATT	CTTCCTTACA	CTCAAATATG	GAATTAATAC	CAAGACATCA
850	860	870	880	890	900
GCCCTAGCAC	TCAGCAGCCT	CACAGGCGAT	ATCCAAAAGA	TGAAGCAGCT	CATGCGTTTA
910	920	930		950	960
TATCGGATGA	AGGGAGAAAA	TGCGCCGTAC		TAGGTGACAG	TGATCAGATG
970 AGCTTTGCAC	980 CGGCTGAGTA		1000 TATTCTTTTG		1020 GGCATCAGTC
1030	1040	1050	1060	1070	1080
TTAGATAAAG	GAACTGGCAA	ATACCAATTC	GCCAGAGACT	TCATGAGCAC	ATCATTCTGG
1090	1100	1110	1120	1130	1140
AGACTCGGGG	TGGAGTATGC	TCAGGCTCAG	GGGAGTAGCA	TCAACGAAGA	CATGGCTGCT
1150 GAGCTAAAAC	1160 TAACCCCGGC		1180 GGCCTGGCAG		1200 ACGAGTGTCT
	1220 GCAGCGTGGA				1260 TGGGCTCAGC
	1280 CCCGAGCCTC				
	1340 AGACCCAATT				
	1400 CCGCACAGAG				
	1460 ACACCGACTG				1500

- 3. (Amended) <A nucleic acid molecule>[Nucleotides] encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).
- 4. (Amended) The [nucleotides as claimed in]<nucleic acid molecule of> claim 3<, wherein the nucleic acid molecule comprises the nucleotide sequence set forth as SEQ ID NO: 2.> [characterised in that it has the following nucleotide sequence:

10	20	30	40	50	60
ATGGCCACCT	TTACAGAȚGC	GGAGATAGAT	GATATATTTG	AGACCAGTGG	AACTGTCATT
70	80	90	100	110	120
GACAGCATAA	TTACGGCCCA	GGGTAAATCA	GCAGAGACTG	TCGGAAGGAG	CGCAATCCCA
130	140	150	160	170	180
CAAGGCAAGA	CCAAAGCGCT	GAGCATAGCA	TGGGAGAAGC	ATGGGAGCAT	CCAACCATCC
190	200	210	220	230	240
ACCAGCCAGG	ACAACCCCGA	CCAACAGGAT	AGACCAGACA	AACAGCTATC	CACACCTGAG
250	260	270	280	290	300
CAGGCGACCC	CACACAACAG	CTCGCCAGCC	ACATCCGCCG	AACCGCTCCC	CACTCAGGCC
310 GCAGGTGAGG	320 CCGGCGACAC	330 ACAGCTCAAG			360 TCTGTCTATG
370	380	390	400	410	420
CTCGACAAGC	TGAGCAATAA	ACCATCTAAT	GCTAAAAAGG	GCCCATGGTC	GAGTCCCCAG
430	440	450	460	470	480
GAAGGATATC	ATCAACCTCC	GACCCAACAA	CATGGGGATC	AGCCGAACCG	CGGAAACAGC
490	500	510	520	530	540
CAGGAGAGGC	TGCGGCACCA	AGCCAAGGCC	GCCCCTGGAA	GCCGGGGCAC	AGACGCGAGC
550	560	570	580		600
ACAGCATATC	ATGGACAATG	GAAGGAGTCA	CAACTATCAG		CCCTCATGTG
610	620	630	640	650	660
CTCCAATCAG	GGCAGAGCCA	AGACAGTACT	CCTGTACCTG	TGGATCATGT	CCAGCCACCT
670	680	690	700	710	720
GTCGACTTTG	TGCAGGCGAT	GATGACTATG	ATGGAGGCGT	TATCACAGAA	GGTAAGTAAA
730	740	750	760	770	780
GTCGACTATC	AGCTAGACCT	AGTCTTAAAG	CAGACATCCT	CCATCCCTAT	GATGCGGTCT
790	800	810	820	830	840
GAAATCCAAC	AGCTAAAAAC	ATCTGTTGCG	GTCATGGAAG	CTAATTTAGG	CATGATGAAA
850	860	870	880	890	900

ATTCTGGACC	CTGGTTGTGC	TAACATTTCA	TCCTTAAGTG	ATCTGCGGGC	AGTCGCCCGG
910	920	930	940	950	960
TCCCACCCAG	TTTTAATTTC	AGGCCCCGGA	GATCCGTCCC	CCTACGTGAC	ACAAGGGGGT
970	980	990	1000	1010	1020
GAGATGACAC	TCAATAAACT	CTCACAACCA	GTACAACACC	CTTCCGAGTT	AATTAAATCT
1030	1040	1050	1060	1070	1080
GCCACAGCGG	GCGGACCTGA	TATGGGAGTG	GAAAAGGACA	CTGTCCGTGC	ATTGATCACC
1090	1100	1110	1120	1130	1140
TCGCGCCCGA	TGCATCCAAG	CTCCTCAGCT	AAGCTCCTGA	GTAAGCTGGA	TGCAGCCGGG
1150	1160	1170	1180	1190	1200
TCGATTGAAG	AGATCAGAAA	GATCAAGCGC	CTTGCACTAA	ATGGCTAA	]

5. (Amended) [The]<A nucleocapsid (NP)> protein <of Newcastle disease virus (NDV) encoded by the nucleic acid molecule>[coded according to] <of> claim 1 or claim 2<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 3.> [characterised in that it has the following amino acid sequence:

1	M ATG 1			GTA		D GAT		TAC		CÃG		L CTC	GCT		~		16
17	R CGC 50					H CAC	GGA			E GAG		-	-		L TTA		32
33		GAG		CCA		F TTC		CTT	AAC		GAC	GAT		GAA			48
49	W TGG					TTC		CTT	R CGG L70			V GTT 180			D GAC	GCC	64
65		AAA		CTC	AGG	Q CAA 210	GGT	GCT	CTC	ATA	TCC	CTC	CTG				80
81	_			ATG	AGG	N AAC	CAT	GTT		CTT				CAG			96
97	A GCT 290	ACA	CTG	ACT	GTT	L CTT	GAG	ATC	GAT	_	TTT		-	-	V GTG		112
113		F TTC			AGG	S AGT	GGG			E GAG	GAG	R AGA 70		CĀG	R AGA 380		128

129	M ATG	V GTG 390	I ATA			TCT	L CTC		R CGG 410	A GCG	C TGC	S AGT 420		G GGT		P CCG 30	144
145	F TTC		T ACG 440	A GCT		V GTT 450		D GAT		A GCA 60	P CCA		D GAT 470	I ATC	T ACT	D GAT 480	160
161	T ACT	L CTG	E GAA 4	R AGA 90				I ATC		A GCT 510		V GTA	TGG	V GTC 20	T ACA	V GTA	176
177			A GCC	M ATG 540	T ACT	GCA	Y TAT 5	GAG	T ACA		D GAT 560	E GAG		E GAA 570		R AGA	192
193			N AAT		Y TAC 590				G GGC		V GTC 61	CAG	K AAG		Y TAC 620	_	208
209	L CTC	H CAC 630	P CCT	V GTA		AGG	S AGT		I ATT 650	Q CAA	L CTC	T ACA 660	I ATC	R AGA	H CAT 6		224
225	L CTG		V GTC 580	R CGC		F TTC 690		V GTT		E GAG DO	L CTT		R AGA 710	G GGC	R CGC	N AAT 720	240
241	T ACG		G GGT 73		-							V GTA			V GTA	_	256
257	S TCA 770	Y TAC	I ATC	R AGG 780	N AAC	ACC				A GCA	TTC	F TTC	L CTT	T ACA 810	L CTC	K AAA	272
257 273	TCA 770 Y	TAC G GGA	ATC	AGG 780 N AAT	AAC T	ACC K	GGA 79 T	CTT 90 S	ACT A	GCA {	TTC 300 A	TTC L CTC	CTT	ACA 810 S AGC	CTC L	AAA T	272
	TCA 770 Y TAT 82	G GGA 20 D	ATC	AGG 780 N AAT	T ACC 330 K	ACC K AAG M ATG	GGA 79 T ACA K	CTT 90 S TCA 840 Q CAG	ACT A GCC L	GCA L CTA	TTC 800 A GCA 85	L CTC 50 L	S AGC	ACA 810 S AGC	CTC L CTC 360 M	T ACA K AAG	
273 289	TCA 770 Y TAT 82 G GGC	G GGA 20 D GAT 870 E GAA	ATC I ATT I ATC	AGG 780 N AAT Q CAA	T ACC 330 K AAG 88	ACC  K AAG  M ATG 30	GGA 79 T ACA K AAG	CTT  S TCA 840  Q CAG	ACT  A GCC  L CTC 390  L TTG	GCA L CTA M ATG	TTC 300 A GCA 85 R CGT	L CTC 60 L TTA 900 D GAC	S AGC Y TAT	ACA 810 S AGC R CGG	L CTC 360 M ATG 91	T ACA  K AAG	288
273 289 305	TCA 770  Y TAT 82  G GGC  G GGA	G GGA 20 D GAT 870 E GAA	ATC I ATT I ATC N AAT	AGG 780  N AAT  Q CAA  A GCG  P CCG	T ACC 330 K AAG 88	ACC  K AAG  M ATG 30  Y TAC 930  E GAG	GGA 75 T ACA K AAG M ATG	CTT O S TCA 840 Q CAG T ACA	ACT  A GCC  L CTC 390  L TTG 94	GCA  L CTA  M ATG  L CTA  10	TTC 300 A GCA 85 R CGT G GGT	L CTC 50 L TTA 900 D GAC	S AGC Y TAT S AGT	ACA 810 S AGC R CGG D GAT	L CTC 360 M ATG 91 Q CAG	T ACA  K AAG 10  M ATG 960	288
<ul><li>273</li><li>289</li><li>305</li><li>321</li><li>337</li></ul>	TCA 770  Y TAT 82  G GGC  G GGA  S AGC	G GGA 20 D GAT 870 E GAA F TTT	ATC I ATT I ATC N AAT 97 GCA 97	AGG 780 N AAT Q CAA A GCG	T ACC 330 K AAG 88 P CCG A GCT	K AAG M ATG 30 Y TAC 930 E GAG D	GGA 79 T ACA K AAG M ATG Y TAT 880 K	CTT S S TCA 840 Q CAG F ACA A GCA GGA	ACT  A GCC  L CTC 390  L TTG 94  Q CAG	GCA  L CTA  M ATG  L CTA  10  L CTT 990  G GGC	TTC 300  A GCA 85  R CGT  G GGT  Y TAT  K	L CTC 60 L TTA 900 D GAC S TCT	S AGC Y TAT S AGT 950 F TTT 100 Q CAA	ACA 810 S AGC R CGG D GAT A GCC	L CTC 360 M ATG 91 Q CAG M ATG	T ACA  K AAG 10  M ATG 960  G GGC	288 304 320
273 289 305 321 337	TCA 770  Y TAT 82  G GGC  G GGA  S AGC  M ATG 010  D	G GGA 20 D GAT 870 E GAA F TTT A GCA	ATC I ATT I ATC N AAT 97 GCA 97	AGG 780  N AAT CAA  A GCG  P CCG 0  V GTC 020  S AGC	T ACC 330 K AAG 88 P CCG A GCT L TTA	ACC  K AAG  M ATG 30  Y TAC 930  E GAG GAT	GGA 79 T ACA  K AAG  M ATG  Y TAT 880  K AAA 103 F TTC	CTT S S TCA 840 Q CAG F ACA A GCA GGA GGA GGA W	ACT A GCC L CTC 390 L TTG 94 CAG T ACT R	GCA  L CTA  M ATG  L CTA  10  L CTT 990  G GGC 10	TTC 300  A GCA 85  R CGT  GGT  Y TAT  K AAA 40 G	L CTC 60 L TTA 9000 D GAC 5 TCT Y TAC V GTG	S AGC Y TAT S AGT 100 Q CAA	ACA 810 S AGC R CGG D GAT A GCC 00 F TTC L050 Y	L CTC 360 M ATG 91 Q CAG M ATG A GCC	AAA  T ACA  K AAG  10  M ATG 960  G GGC  R AGA	288 304 320

385		CCG	A GCA 160	GCA	AGA	AGG	GGC	CTG	GCA	GCT	GCT	GCC	CAA		GTG		400
401			ACT	GGC	AGC	GTG		ATT	CCT	ACT	CAA	CAA	GCC	GGG		L CTC	416
	т АСТ 250	GGG	CTC	AGC	GAT	GGA	GGC	CCC	CGA	GCC	TCT	CAG	GGT	GGA			432
433	AAG	TCG	Q CAA	GGG	CAA	CCA	GAT	GCC	GGA	GAT	GGG	GAG	ACC	CAA	TTC		448
449		TTG	M ATG	AGA	GCA	GTG	GCG	AAC	AGC	ATG	CGA	GAA	GCG		AAC	TCC	464
465	A GCA	CĀG	S AGC 400	ACC	ACC	CAC	CCG	GAA	CCC	CCC	CCG	ACT			CCA		480
481	Q CAA		AAC	GAC	ACC		TGG	GGG		TGA							490 ]

6. (Amended) [The] <A phosphoprotein (P)> protein <of Newcastle disease virus (DNV) encoded by the nucleic acid molecule> [coded according to] <of> claim 3 or claim 4<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 4.> [characterised in that it has the following amino acid sequence:

1	M ATG 1	A GCC		F TTT 10	T ACA	D GAT	A GCG 20	E GAG	I ATA	D GAT 30	D GAT	I ATA		E GAG 10	T ACC	S AGT	16
17	G GGA 50	T ACT	V GTC	I ATT 60	D GAC	S AGC	I ATA	I ATT 70		A GCC	Q CAG 80	G GGT	K AAA	S TCA 90		E GAG	32
33	T ACT		G GGA		S AGC 110		I ATC						K AAA		L CTG L40	S AGC	48
49		A GCA 150	W TGG	E GAG		H CAT 50	G GGG	AGC	I ATC 170	-			T ACC	S AGC		D GAC 90	64
65	N AAC		D GAC 200	Q CAA	Q CAG		R AGA		GAC		Q CAG		S TCC 230	T ACA	P CCT	E GAG 240	80
81	Q CAG	A GCG		P CCA 50	H CAC		S AGC 260		P CCA	A GCC 270	T ACA	S TCC		E GAA 30	P CCG	L CTC	96

97		ACT	-	A GCC 300	A GCA	G GGT	E GAG 31		G GGC	GAC	T ACA 320	_			T ACC		112
113	GCA	-	N AAC				S TCT		L CTC				S AGC			P CCA	128
129				K AAA		GGC	P CCA	TGG		S AGT	P CCC	_	E GAA	G GGA	Y TAT 4		144
145	-	CCT	P CCG 440				H CAT	GGG	D GAT 4	CAG			CGC	G GGA	N AAC	-	160
161	Q CAG		AGG			CAC	Q CAA 500						GGA				176
177	T ACA 530	_	GCG	S AGC 540		GCA	Y TAT 55	CAT	GGA	Q CAA	TGG		E GAG			L CTA	192
193				A GCA	ACC		H CAT		CTC		S TCA 61	GGG	Q CAG				208
209	S AGT					GTG	D GAT	CAT	V GTC 650		P CCA				F TTT 6	GTG	224
225	Q CAG	GCG		M ATG	ACT		ATG	GAG				CÃG			-	K AAA 720	240
241	V GTC			CAG		GAC	L CTA 740		L TTA		_	T ACA		TCC	I ATC	P CCT	256
257	770	M ATG		S TCT 780	E GAA	I ATC	Q CAA 79			K AAA 8		S TCT	V GTT		V GTC	M ATG	272
273		GCT	N AAT	TTA	G GGC 330		M ATG	K AAA 840		L CTG				TGT			288
289		S TCA 870			S AGT 88	GAT	L CTG			V GTC		R CGG 900					304
305	L TTA		S TCA 920	G GGC	P CCC		D GAT	P CCG			Y TAC			Q CAA	G GGG	G GGT 960	320
321	E GAG		ACA	L CTC			L CTC 980		_	P CCA 990		Q CAA			S TCC	E GAG	336
337	L TTA	I ATT	K AAA	S TCT	A GCC	T ACA	A GCG	G GGC	G GGA	P CCT	D GAT	M ATG	G GGA	V GTG	E GAA	K AAG	352

1	010		1	1020			103	30		10	040		:	1050			
353	D GAC	T ACT	V GTC	R CGT	A GCA	L TTG	_	T ACC	S TCG		P CCG	M ATG	H CAT	P CCA	S AGC	S TCC	368
	10	60		10	070		:	1080			109	90		1:	100		
369	s	Α	K	L	L	s	K	L	D	A	A	G	s	r	E	E	384
	TCA	GCT	AAG	CTC	CTG	AGT	AAG	CTG	GAT	GCA	GCC	GGG	TCG	ATT	GAA	GAG	
	:	1110			112	20		1:	130		1	1140			115	50	
385	I	R	K	I	K	R	L	Α	L	N	G	*					396
	ATC	AGA	AAG	ATC	AAG	CGC	CTT	GCA	CTA	AAT	GGC	TAA					
		13	L 60		1	170			118	30							]

15. (Amended) A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 3.> [characterised in that it has the following amino acid sequence:

1		S TCT	TCC		F TTC								GCT				16
17					A GCT		GGA								L TTA		32
33	GTT			CCA	V GTA 110					S AGT		GAT		GAA	D GAT 140		48
49				GCG	V GTA	TTC	TGT		CGG						GAC	A GCC 90	64
65	N AAC	AAA			R AGG			GCT		ATA		CTC					80
81	-	_	GTG		R AGG	AAC								CAG			96
97	A GCT 290	ACA	CTG	ACT	GTT		GAG	ATC		GGT	TTT				V GTG		112
113	Q CAG 34	TTC	AAC		AGG		GGG	GTG	TCT	GAG	GAG	AGA	GCA	_			128
129	M ATG		ATA	GCA	G GGG 40	TCT	CTC	CCT	CGG			AGT	AAC	GGT	T ACT 43	CCG	144
145	F TTC		_		G GGG	V GTT				A GCA			D GAT	_	T ACT	_	160

	4	440		450			4 (	60			470			480	
161	T L ACT CTG	E GAA A 490	GA ATC					A GCT 510	Q CAG	V GTA	TGG	V GTC 20	_		176
177	A K GCG AAG 530	GCC A	M T TG ACT 40						D GAT 560	E GAG	S TCG	E GAA 570	T ACA	R AGA	192
193	R I AGA ATC 580		K Y AG TAC 590		_	_	G GGC		GTC	~	K AAG		Y TAC 520	_	208
209	L H CTC CAC 630		V C TA TGC 6	AGG		GCA	I <b>ATT</b> 650	-			I ATC		H CAT 67	TCT	224
225	L A CTG GCA		R I GC ATT						L CTT		R AGA 710	G GGC	R CGC	N AAT 720	240
241	T A ACG GCA	_	GG AGC				TAC		L TTA	V GTA	_			D GAC	256
257	S Y TCA TAC 770				G GGA 79	CTT		GCA				T ACA 810		K AAA	272
273	Y G TAT GGA 820			K AAG				L CTA	GCA	L CTC 50	S AGC				288
289	G D GGC GAT 870	ATC C	Q K AA AAG 8	ATG	AAG	Q CAG	CTC	M ATG	R CGT	L TTA 900	Y TAT	R CGG			304
305	G E GGA GAA			Y TAC 930					G GGT		S AGT 950	D GAT	Q CAG	M ATG 960	320
321	S F AGC TTT				Y TAT 086	A GCA	Q CAG	L CTT 990	Y TAT	S TCT	F TTT 100		M ATG	G GGC	336
	M A ATG GCA .010		TC TTA			GGA		GGC			CAA				352
353	D F GAC TTC 1060	ATG A			TTC					GTG		TAT			368
369	A Q GCT CAG 1110		GT AGC	ATC		GAA	GAC		GCT		GAG			CTA	384
385	T P ACC CCG 11		CA AGA					GCT		GCC			GTG		400
401	E E	T	g s	v	D	I	P	T	Q	Q	A	G	v	L	416

	GAG	GAA	ACT	GGC	AGC	GTG	GAT	ATT	CCT	ACT	CAA	CAA	GCC	GGG	GTC	CTC	
			123	LO		12	220		:	1230			12	40			
417	т	G	τ.	s	מ	G	G	P	R	Δ	s	0	G	G	s	N	432
						GGA											
1	250		1	1260			12	70		12	280		:	1290			
133	К	c	0	c	0	D	ח	7	c	D	C	Ė	TT.	^	E	T	448
433						CCA								_			440
						0011										110	
				_`			•										
449	D	L	M	R	Α	V	Α	N	S	M	R	Ė	Α	P	N	S	464
	GAT	TTG	ATG	AGA	GCA	GTG	GCG	AAC	AGC	ATG	CGA	GAA	GCG	CCA	AAC	TCC	
	1	1350			13	60		13	370			1380			139	90	
465	А	0	S	т	т	н	P	E.	P	P	P	т	P	G	P	s	480
		~				CAC				_	-	_	_	-	_	_	
		14	100			1410			142	20		14	130			1440	
481	Q	D	N	D	T	D	W	G	Y	*							490
	CAA	GAT				GAC											
			145	50		14	160		:	L470							]

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16. (Amended) A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 4.> [characterised in that it has the following amino acid sequence:

1	M ATG 1	A GCC		F TTT 10	T ACA	D GAT	A GCG 20	E GAG	I ATA	D GAT 30	D GAT	I ATA		E GAG 10	T ACC	S AGT	16
17	G GGA 50	T ACT	V GTC	I ATT 60	D GAC	S AGC		I ATT 70	T ACG	A GCC	Q CAG 80	G GGT	K AAA	S TCA 90		E GAG	32
33		V GTC 00		AGG		A GCA						ACC		GCG		S AGC	48
49	I ATA	A GCA 150	W TGG	E GAG	K AAG 1	H CAT 50	G GGG	AGC	I ATC L70	Q CAA	P CCA	S TCC 180	T ACC	S AGC		D GAC 90	64
65	N AAC		D GAC 200	Q CAA		D GAT 210			GAC			CTA	S TCC 230		P CCT	_	80
81	Q CAG	A GCG		P CCA 50	H CAC	N AAC	s AGC 260		P CCA		T ACA	S TCC	A GCC 28		P CCG	L CTC	96
97	P CCC 290	T ACT	Q CAG	A GCC 300	A GCA	G GGT		A GCC L0	G GGC		T ACA 320	Q CAG	L CTC	K AAG 330	T ACC	G GGA	112

113	GCA	S AGC 40	N AAC			L C <b>TG</b>	S TCT	M ATG 360			K AAG 3	CTG	S AGC	AAT	K AAA 380		128
129		N AAT 390				GGC	P CCA	TGG				Q CAG 420			TAT		. 144
145	~	CCT			CAA	Q CAA 450		G GGG		CAG			CGC				160
161	_	E GAG	R AGG 45	CTG								PCCT	GGA			G GGC	176
177	T ACA 530	D GAC						CAT		CAA					_	L CTA	192
193	S TCA 58	GCT		A GCA	ACC	P CCT	CAT				S TCA 6:	GGG				D GAC	208
209	S AGT	T ACT 630						CAT	GTC	-		P CCT 660			F TTT 6	GTG	224
225		A GCG			T ACT		M ATG		A GCG 7(	TTA					S AGT		240
241		D GAC		CAG	CTA						CAG			TCC	I ATC	_	256
257	M ATG 770	M ATG	R CGG		E GAA		Q CAA 79	CAG						A GCG 810		M ATG	272
273	E GAA 82	GCT	N AAT	L TTA		M ATG		K AAA 840	I ATT		D GAC 85	CCT	G GGT		A GCT 860	N AAC	288
289	I ATT	S TCA 870			AGT		L CTG	CGG							CCA		304
305	L											V GTG		_	G		320
	TTA		TCA 920	GGC	CCC	930	GAT	CCG	94		IAC		50	CAA	GGG	960	
321	E	9	T ACA	L	N	930 K AAA	L	s	94 Q	10 P	v	Q	950 H	P CCT	S	960 E	336
337	E GAG L	M ATG	T ACA 97 K AAA	L CTC 70	N AAT A	930 K AAA T	L CTC 980 A	S TCA G GGC	Q CAA G	P CCA 990 P CCT	V GTA D	Q CAA M	H CAC 100 G GGA	P CCT OO V	S TCC E	960 E GAG K	336 352

	1060			10	070		:	1080			109	90	1100					
369	s	Α	K	L	L	s	K	L	D	Α	Α	G	s	I	E	E	384	
	TCA	GCT	AAG	CTC	CTG	AGT	AAG	CTG	GAT	GCA	GCC	GGG	TCG	ATT	GAA	GAG		
	1110				1120			1130			1140				11	50		
385	I	R	ĸ	I	K	R	L	A	L	N	G	*					396	
	ATC	AGA	AAG	ATC	AAG	CGC	CTT	GCA	CTA	AAT	GGC	TAA						
	1160				1170			1180			30						]	